

# SEQUENCE LISTING

<110> Shi, Jinrui  
Beach, Larry  
Wang, Hongyu  
Rafalski, Antoni J.  
Rebecca E. Cahoon

<120> Novel Inositol Polyphosphate Kinase  
Genes and Uses Thereof

<130> 1286

<150> US 60/261,465

<151> 2001-01-12

<160> 37

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1169

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (84)...(806)

<400> 1

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cttgctccca tagtccccat acc atg ccc gac ctc cac ccg ccg gag cac caa      113
                               Met Pro Asp Leu His Pro Pro Glu His Gln
                               1               5               10

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gtc gcc ggt cac cgc gcc tcc gcc agc aag ctg ggc ccg ctc atc gac      161
Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp
                               15               20               25

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ggc tcc ggc ctc ttc tac aag ccg ctc cag gcc ggc gac cgt ggg gag      209
Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu
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cac gag gtc gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc gtc ccg      257
His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala Val Pro
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gcc cgc atc cga gac acc ttc ttc ccc ccg ttc cac ggc acg cga ctc      305
Ala Arg Ile Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr Arg Leu
                               60               65               70

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ctc ccc acc gag gcg cag ccc ggg gag ccg cat ccg cac ctc gtc ctc      353
Leu Pro Thr Glu Ala Gln Pro Gly Glu Pro His Pro His Leu Val Leu
                               75               80               85               90

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gac gac ctc ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac atc aag      401
Asp Asp Leu Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp Ile Lys

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	95		100		105	
atc ggc gcc atc acg tgg cca cgg agt tgc cgg gag ccc tac atc gcc						449
Ile Gly Ala Ile Thr Trp Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala						
	110		115		120	
aag tac ctc gcc aag gac cgc ggg acc acg agc gtt ctg ctc gga ttc						497
Lys Tyr Leu Ala Lys Asp Arg Gly Thr Thr Ser Val Leu Leu Gly Phe						
	125		130		135	
cgc gtc ttg cgt cgg agt cgt cgg ccc cga ggg cgc cgt gtg gcg gac						545
Arg Val Leu Arg Pro Ser Arg Arg Pro Arg Gly Arg Arg Val Ala Asp						
	140		145		150	
gga cgc ccc gga ggt gaa ggc tat gga cac cgt cgg cgt cgc cgc cgt						593
Gly Ala Pro Gly Gly Glu Gly Tyr Gly His Arg Arg Pro Pro Arg						
	155		160		165	170
gct cgc gcg cta cgt gtc atc cgc ttg cgg acg agg gga tgg act gcg						641
Ala Pro Ala Leu Arg Val Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala						
	175		180		185	
cgc tgc cgg cgg cgg tgt acg gag gaa aag gtg gag tct tgt cac agc						689
Arg Ser Arg Arg Arg Cys Thr Glu Glu Lys Val Glu Ser Cys His Ser						
	190		195		200	
tgc gcg agc tca agg cat ggt tgg agg agc aga ctc tgt tcc act tct						737
Cys Ala Ser Ser Arg His Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser						
	205		210		215	
act cgg cgt cga ttc ttc tgg gct atg atg ctg ctg cag tgc cag cag						785
Thr Arg Arg Arg Phe Thr Trp Ala Met Met Leu Leu Gln Ser Gln Gln						
	220		225		230	
gcg gag gtg ggg gtg ggg taa cagtgaagct ggtggacttt gcccatgtgg						836
Ala Glu Val Gly Val Gly *						
	235		240			
ccgagggtga tgggggtgatt gaccacaact tcttgggcga gctctgctag ctgatcaagt						896
tcgtttctga cattgttcca gagactcctt agacgcagcc ttgggtcct tcttaagaga						956
ggatcctgac atttttgatt tgataacaaa ggaagcactt tcagctgcaa aaaaagaaag						1016
cagcagtgag gatgaagatg acagtagtga ggaagttcg gatgatgagc caacaaaagt						1076
tgaagaaaag aaggctccaa aagtatcaga aaacattgga tctgaggatg aatcttctga						1136
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Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala						
1 5 10 15						
Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr						
20 25 30						
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr						
35 40 45						
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr						

50	Phe	Arg	Pro	Arg	Phe	His	Gly	Thr	Arg	Leu	Leu	Pro	Thr	Glu	Ala	Gln
65	Pro	Gly	Glu	Pro	His	Pro	His	Leu	Val	Leu	Asp	Asp	Leu	Leu	Ala	Gly
					85					90					95	
	Phe	Glu	Ala	Pro	Cys	Val	Ala	Asp	Ile	Lys	Ile	Gly	Ala	Ile	Thr	Trp
					100					105					110	
	Pro	Pro	Ser	Ser	Pro	Glu	Pro	Tyr	Ile	Ala	Lys	Tyr	Leu	Ala	Lys	Asp
					115					120					125	
	Arg	Gly	Thr	Thr	Ser	Val	Leu	Leu	Gly	Phe	Arg	Val	Leu	Arg	Pro	Ser
					130					135					140	
	Arg	Arg	Pro	Arg	Gly	Arg	Arg	Val	Ala	Asp	Gly	Ala	Pro	Gly	Gly	Glu
					145					150					155	
	Gly	Tyr	Gly	His	Arg	Arg	Arg	Pro	Pro	Arg	Ala	Pro	Ala	Leu	Arg	Val
					165					170					175	
	Ile	Arg	Leu	Pro	Thr	Arg	Gly	Trp	Thr	Ala	Arg	Ser	Arg	Arg	Arg	Cys
					180					185					190	
	Thr	Glu	Glu	Lys	Val	Glu	Ser	Cys	His	Ser	Cys	Ala	Ser	Ser	Arg	His
					195					200					205	
	Gly	Trp	Arg	Ser	Arg	Leu	Cys	Ser	Thr	Ser	Thr	Arg	Arg	Arg	Phe	Phe
					210					215					220	
	Trp	Ala	Met	Met	Leu	Leu	Gln	Ser	Gln	Gln	Ala	Glu	Val	Gly	Val	Gly
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<211> 923

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (53)...(736)

<400> 3

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							1	
gac	ctc	cac	ccg	ccg	gag	cac	caa	gtc
Asp	Leu	His	Pro	Pro	Glu	His	Gln	Val
								10
								15
gag	ctc	cac	ccg	ccg	ctc	atc	gac	ggc
Ser	Lys	Pro	Gly	Pro	Leu	Ile	Asp	Gly
								25
								30
ctc	cag	gcc	ggc	gac	cgt	ggg	gag	cac
Leu	Gln	Ala	Gly	Asp	Arg	Gly	Glu	His
								40
								45
ttc	ttc	gcc	cac	gcc	gcc	gtc	ccg	gcc
Phe	Ser	Ala	His	Ala	Ala	Val	Pro	Ala
								55
								60
ccc	acc	gag	gag	gag	ccc	acc	gag	gag
Pro	Arg	Phe	His	Gly	Thr	Arg	Leu	Leu
								70
								75
								80

gag ccg cat ccg cac ctc gtc ctc gac gac ctc ctc gcg gga ttt gag 346  
 Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Glu  
 85 90 95

gcg ccc tgc gtc gca gac atc aag atc ggc gcc atc acg tgg cca ccg 394  
 Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro  
 100 105 110

agt tgc ccg gag ccc tac atc gcc aag tgc ctc gcc atg gac cgc ggg 442  
 Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp Arg Gly  
 115 120 125 130

acc acg agc gtt ctg ctc gga ttc cgc gtc tcc ggc gtc cga gtc gtc 490  
 Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg Val Val  
 135 140 145

gtc ccc gag ggc gcc gtg tgg cgg acg gag cgc ccg gag gtg aag gct 538  
 Val Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala  
 150 155 160

atg gac acc gtc ggc gtc cgc cgc gtg ctc cgg cgc tac gtg tca tcc 586  
 Met Asp Thr Val Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser  
 165 170 175

gct tgc cga cga ggg gat gga ctg cgc gct cgc ggc ggc ggt gta cgg 634  
 Ala Cys Arg Arg Gly Asp Gly Leu Arg Ala Arg Gly Gly Val Arg  
 180 185 190

agg aaa agg tgg agt ctt gtc act gct gcg cga gct caa ggc gtg gtt 682  
 Arg Lys Arg Trp Ser Leu Val Thr Ala Ala Arg Ala Gln Gly Val Val  
 195 200 205 210

cga gga gca gcc tct gtt cca ctt cta ctc ggc gtc gat tct tct ggg 730  
 Arg Gly Ala Ala Ser Val Pro Leu Leu Gly Val Asp Ser Ser Gly  
 215 220 225

cta tga tgctgctgca gtcgcagcag gcggaggtgg ggggtgggta acagtgaagc 786  
 Leu \*

tggtggactt tgcccatgtg gcgaggggtg atgggggtgat tgaccacaac ttctctgggcg 846  
 ggctctgcta gctgatcaag ttcgtttctg acattgttcc agagactcct cagacgcagc 906  
 ctttgggtcc ttcttaa 923

&lt;210&gt; 4

&lt;211&gt; 227

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;400&gt; 4

Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala  
 1 5 10 15  
 Ser Ala Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr  
 20 25 30  
 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
 35 40 45  
 Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr

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<220>
<221> CDS
<222> (53) ... (922)
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                                     Met Pro
                                     1

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gac ctc cac ccg ccg gag cac caa gtc gcc ggt cac cgc gcc tcc gcc 106  
Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala  
5 10 15

agc aag ccg ggc ccg ctc atc gac ggc tcc ggc ctc ttc tac aag ccg 154  
 Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro  
 20 25 30

ctc cag gcc ggc gac cgt ggg gag cac gag gtc gct ttc tat gag gcg 202  
Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala  
35 40 45 50

ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc cga gac acc ttc ttc 250  
Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe  
55 60 65

ccc cgg ttc cac ggc acg cga ctc ctc ccc acc gag gcg cag ccc ggg 298  
Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly  
70 75 80

gag ccg cat ccg cac ctc gtc ctc gac gac ctc ctc gcg gga ttt gag Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Glu 85 90 95	346
gcg ccc tgc gtc gca gac atc aag atc ggc gcc atc acg tgg cca ccg Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro 100 105 110	394
agt tgc ccg gag ccc tac atc gcc aag tgc ctc gcc atg gac cgc ggg Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys 125 115 120 125	442
acc acg agc gtt ctg ctc gga ttc cgc gtc tcc gcc gtc cga gtc gtc Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg Val Val 135 140 145	490
ggc ccc gag gcc gcc gtg tgg cgg acg gag cgc ccg gag gtg aag gcc Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala 150 155 160	538
atg gac acc gcc gcc gtc cgc cgc gtg ctc cgg cgc tac gtg tca tcc Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser 165 170 175	586
gtt gcc gac gag ggg atg gac tgt gcg ctc gcc gcg gcg gtg tac gga Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val Tyr Gly 180 185 190	634
gga aaa ggt gga gtc ttg tca cag ctg cgc gag ctc aag gcg tgg ttc Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala Trp Phe 195 200 205 210	682
gag gag cag act ctg ttc cac ttc tac tcg gcg tcg att ctt ctg gcc Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu Leu Gly 215 220 225	730
tat gat gct gct gca gtc gca gca gcc gga ggt ggg ggt ggg gtg acg Tyr Asp Ala Ala Val Ala Ala Gly Gly Gly Gly Gly Val Thr 230 235 240	778
gtg aag ctg gtg gac ttt gcc cat gtg gcc gag ggt gat ggg gtg att Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly Val Ile 245 250 255	826
gac cac aac ttc ctg gcc ggg ctc tgc tcg ctg atc aag ttc gtt tct Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe Val Ser 260 265 270	874
gac att gtt cca gag act cct cag acg cag cct ttg ggt cct tct taa Asp Ile Val Pro Glu Thr Pro Gln Thr Gln Pro Leu Gly Pro Ser * 275 280 285	922
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<213> Zea mays

<400> 6

Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala  
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 Ser Ala Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr  
 20 25 30  
 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
 35 40 45  
 Glu Ala Phe Ser Ala His Ala Val Pro Ala Arg Ile Arg Asp Thr  
 50 55 60  
 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
 65 70 75 80  
 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly  
 85 90 95  
 Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp  
 100 105 110  
 Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp  
 115 120 125  
 Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg  
 130 135 140  
 Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val  
 145 150 155 160  
 Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val  
 165 170 175  
 Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val  
 180 185 190  
 Tyr Gly Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala  
 195 200 205  
 Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu  
 210 215 220  
 Leu Gly Tyr Asp Ala Ala Val Ala Ala Gly Gly Gly Gly Gly Gly  
 225 230 235 240  
 Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly  
 245 250 255  
 Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe  
 260 265 270  
 Val Ser Asp Ile Val Pro Glu Thr Pro Gln Thr Gln Pro Leu Gly Pro  
 275 280 285  
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<210> 7

<211> 1344

<212> DNA

<213> Zea mays

<220>

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<222> (52) ... (921)

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57

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105

Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala  
 5 10 15  
 agc aag ctg ggc cgc ctc atc gac ggc tcc ggc ctc ttc tac aag ccg 153  
 Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro  
 20 25 30  
 ctc cag gcc ggc gac cgt ggg gag cac gag gtc gcc ttc tat gag gcg 201  
 Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala  
 35 40 45 50  
 ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc cga gac acc ttc ttc 249  
 Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe  
 55 60 65  
 ccc cgg ttc cac gcc acg cga ctc ctc ccc acc gag gcg cag ccc ggg 297  
 Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly  
 70 75 80  
 gag ccg cat cct cac ctc gtc ctc gac gac ctc ctc gcg ggg ttt cag 345  
 Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Gln  
 85 90 95  
 gcg ccc tgc gtc gca gac atc aag atc ggc gcc atc acg tgg cca ccg 393  
 Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro  
 100 105 110  
 agt tgg ccg gag ccc tac atc gcc aag tgc ctc gcc aag gac cgc ggg 441  
 Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Lys Asp Arg Gly  
 115 120 125 130  
 acc acg agc gtt ctg ctc gga ttc cgc gtc tcc ggc gtc cga gtc gtc 489  
 Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg Val Val  
 135 140 145  
 ggc ccc gag ggc gcc gtg tgg cgg acg gag cgc ccg gag gtg aag gcc 537  
 Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala  
 150 155 160  
 atg gac acc gcc ggc gtc cgc cgc gtg ctc cgg cgc tac gtg tca tcc 585  
 Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser  
 165 170 175  
 gtt gcc gac gag ggg atg gac tgt gcg ctc gcc gcg gcg gtg tac gga 633  
 Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val Tyr Gly  
 180 185 190  
 gga aaa ggt gga gtc ttg tca cag ctg cgc gag ctc aag gcg tgg ttc 681  
 Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala Trp Phe  
 195 200 205 210  
 gag gag cag act ctg ttc cac ttc tac tgg gcg tgg att ctt ctg gcc 729  
 Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu Leu Gly  
 215 220 225  
 tat gat gct gct gca gtc gca gca gcc gga gat ggg ggt ggg gtg acg 777  
 Tyr Asp Ala Ala Val Ala Ala Gly Gly Asp Gly Gly Gly Val Thr  
 230 235 240



gtg aag ctg gtg gac ttt gcc cat gtg gcc gag ggt gat ggg gtg att 825  
Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly Val Ile  
245 250 255

gac cac aac ttc ctg ggc ggg ctc tgc tgc ctg atc aag ttc gtt tct 873  
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe Val Ser  
260 265 270

gac att gtt ccg gag act cct cat acg cag cct ttg ggt cct tct taa 921  
Asp Ile Val Pro Glu Thr Pro His Thr Gln Pro Leu Gly Pro Ser \*  
275 280 285

gagaggatcc tggcattctg atttgataac aaagccctac aagttttgtc tggaaaaaga 981  
agcgctctcg agttgtgctg ggtgtggaga tctgagacgg tcgtcgccccc acttggttgc 1041  
cttgccctttg ccttgccctgc aaacatacgg caacctgtctc cttttttcgc aaccctctac 1101  
ttccgaagaa actttttttt tcccactttg ggggttcgat tacgtttggat ctggtttgtg 1161  
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ctttgcgtg cctgcgcttt ctgcatggct tttgcctgct gcgacccgat gtgtactgga 1281  
gatcgtagtg atggacgtct ctacctccaa acgaatccgt ccgataaaaa aaaaaaaaaa 1341  
aaa 1344

<210> 8  
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<212> PRT  
<213> Zea mays

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Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr  
20 25 30  
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
35 40 45  
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr  
50 55 60  
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
65 70 75 80  
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly  
85 90 95  
Phe Gln Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp  
100 105 110  
Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Lys Asp  
115 120 125  
Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg  
130 135 140  
Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val  
145 150 155 160  
Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val  
165 170 175  
Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val  
180 185 190  
Tyr Gly Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala  
195 200 205  
Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu  
210 215 220  
Leu Gly Tyr Asp Ala Ala Val Ala Ala Gly Gly Asp Gly Gly Gly  
225 230 235 240

Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly  
 245 250 255  
 Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe  
 260 265 270  
 Val Ser Asp Ile Val Pro Glu Thr Pro His Thr Gln Pro Leu Gly Pro  
 275 280 285  
 Ser

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 <212> DNA  
 <213> Glycine max

<220>  
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 Met Leu Lys Ile Pro Glu His Gln Val Ala Gly His Lys  
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 gcc aag gac gga atc ctg gcc cca ctc gtc gac gat ttt gga aaa ttc 98  
 Ala Lys Asp Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe  
 15 20 25  
 tac aag ccc ctc cag acc aac aaa gac gac gac acc cgc gcc tcc acc 146  
 Tyr Lys Pro Leu Gln Thr Asn Lys Asp Asp Thr Arg Gly Ser Thr  
 30 35 40 45  
 gaa ctc tcc ttt tac acc tct ctc gcc gcc gcc gcc cac gac tac tcc 194  
 Glu Leu Ser Phe Tyr Thr Ser Leu Ala Ala Ala Ala His Asp Tyr Ser  
 50 55 60  
 atc cgc tcc ttc ttc ccc gcc ttt cac gcc acc cgc ctc ctg gac gcc 242  
 Ile Arg Ser Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala  
 65 70 75  
 tcc gac gcc tcc ggt ccc cac cct cac ctg gtc ctg gag gac ctc ctc 290  
 Ser Asp Gly Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu  
 80 85 90  
 tgc gcc tac tcc aaa ccc tcc gtc atg gac gta aag atc gcc tcc aga 338  
 Cys Gly Tyr Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg  
 95 100 105  
 acc tgg cac ctg gga gac tcc gag gac tac atc tgc aag tgc ctg aag 386  
 Thr Trp His Leu Gly Asp Ser Glu Asp Tyr Ile Cys Lys Cys Leu Lys  
 110 115 120 125  
 aag gac aga gag tcc tct agc ttg ccc ttg ggt ttc aga atc tgc gga 434  
 Lys Asp Arg Glu Ser Ser Ser Leu Pro Leu Gly Phe Arg Ile Ser Gly  
 130 135 140  
 gtc aag gac tct atc tcc tcc tgg gaa cct acc agg aaa tct ctc cag 482  
 Val Lys Asp Ser Ile Ser Ser Trp Glu Pro Thr Arg Lys Ser Leu Gln  
 10

10042894.010902

145 150 155

tgt cta tcc gcc cat ggt gtt gca ctt gtt ctc aac aag ttc gtt tcc 530  
Cys Leu Ser Ala His Gly Val Ala Leu Val Leu Asn Lys Phe Val Ser  
160 165 170

tct aat aat atc aac cat gat gat cat cat ccc gat tgc gct ttc gca 578  
Ser Asn Asn Ile Asn His Asp Asp His His Pro Asp Cys Ala Phe Ala  
175 180 185

acg gag gtc tac gcc gcc gtt ttg gag cgc ttg cag aag ctc aag gac 626  
Thr Glu Val Tyr Gly Ala Val Leu Glu Arg Leu Gln Lys Leu Lys Asp  
190 195 200 205

tgg ttc gag gtt cag acg gtg tat cac ttc tat tct tgt tct gtt ctt 674  
Trp Phe Glu Val Gln Thr Val Tyr His Phe Tyr Ser Cys Ser Val Leu  
210 215 220

gtg gtg tac gag aag gat cta ggg aaa ggg aaa gct acc aac cct ctg 722  
Val Val Tyr Glu Lys Asp Leu Gly Lys Gly Lys Ala Thr Asn Pro Leu  
225 230 235

gtc aaa ctc gtt gac ttt gca cac gtg gtg gac gga aac ggt gtc att 770  
Val Lys Leu Val Asp Phe Ala His Val Val Asp Gly Asn Gly Val Ile  
240 245 250

gat cac aac ttc ttg ggt gcc ctt tgt tcc ttc atc aag ttc ctc aag 818  
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Phe Ile Lys Phe Leu Lys  
255 260 265

gat atc cta gca gta gca tgt ctt cac aag tga ctgattttca tcgagttaat 871  
Asp Ile Leu Ala Val Ala Cys Leu His Lys \*  
270 275

cttattccta tcagaaaata attatgcttg aattagtgtc gcagactaac tgtttgaagt 931  
actgtcagaa acaaaaataa aatatggact gagaggcaat ctgttcttgc taaactccct 991  
ttcaagttgc tgtcagatac tagcgtccc ttttctcttt tcatattctg tcaagtgtag 1051  
tcatttaata ataatacaaa tgtccttcaa ctccaaaaaa aaaaaaaaaa aaaa 1105

<210> 10  
<211> 279  
<212> PRT  
<213> Glycine max

<400> 10  
Met Leu Lys Ile Pro Glu His Gln Val Ala Gly His Lys Ala Lys Asp  
1 5 10 15  
Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe Tyr Lys Pro  
20 25 30  
Leu Gln Thr Asn Lys Asp Asp Asp Thr Arg Gly Ser Thr Glu Leu Ser  
35 40 45  
Phe Tyr Thr Ser Leu Ala Ala Ala His Asp Tyr Ser Ile Arg Ser  
50 55 60  
Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala Ser Asp Gly  
65 70 75 80  
Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu Cys Gly Tyr  
85 90 95  
Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg Thr Trp His

100 105 110  
 Leu Gly Asp Ser Glu Asp Tyr Ile Cys Lys Cys Leu Lys Lys Asp Arg  
 115 120 125  
 Glu Ser Ser Ser Leu Pro Leu Gly Phe Arg Ile Ser Gly Val Lys Asp  
 130 135 140  
 Ser Ile Ser Ser Trp Glu Pro Thr Arg Lys Ser Leu Gln Cys Leu Ser  
 145 150 155 160  
 Ala His Gly Val Ala Leu Val Leu Asn Lys Phe Val Ser Ser Asn Asn  
 165 170 175  
 Ile Asn His Asp Asp His His Pro Asp Cys Ala Phe Ala Thr Glu Val  
 180 185 190  
 Tyr Gly Ala Val Leu Glu Arg Leu Gln Lys Leu Lys Asp Trp Phe Glu  
 195 200 205  
 Val Gln Thr Val Tyr His Phe Tyr Ser Cys Ser Val Leu Val Val Tyr  
 210 215 220  
 Glu Lys Asp Leu Gly Lys Gly Lys Ala Thr Asn Pro Leu Val Lys Leu  
 225 230 235 240  
 Val Asp Phe Ala His Val Val Asp Gly Asn Gly Val Ile Asp His Asn  
 245 250 255  
 Phe Leu Gly Gly Leu Cys Ser Phe Ile Lys Phe Leu Lys Asp Ile Leu  
 260 265 270  
 Ala Val Ala Cys Leu His Lys  
 275

<210> 11  
 <211> 1195  
 <212> DNA  
 <213> Eucalyptus grandis

<220>  
 <221> CDS  
 <222> (116) ... (1048)

<400> 11  
 gcaccagctt cttggagtag ttgcccatca gcgtggattt tcatttttagt ccattctggct 60  
 gtgatcaatc gaattctgagt aagtttggag aattttttcg cacatcagat acacc atg 118  
 Met  
 1  
 ctc aag gtc cgg gat cat caa gtc gcc ggt cac cgg gga gac ggg gga 166  
 Leu Lys Val Pro Asp His Gln Val Ala Gly His Arg Gly Asp Gly Gly  
 5 10 15  
 aag ctg ggg cca ctg gtg gat gat tcg ggc cgc ttc tat aag cct ctc 214  
 Lys Leu Gly Pro Leu Val Asp Ser Gly Arg Phe Tyr Lys Pro Leu  
 20 25 30  
 cag agc gat cat cgc gga gac acg gaa gtg gcc ttt tac gag tca ttc 262  
 Gln Ser Asp His Arg Gly Asp Thr Glu Val Ala Phe Tyr Glu Ser Phe  
 35 40 45  
 tat tcc aat acc gag atc cca ggt cac att cgc aaa ttc ttt cct gcg 310  
 Tyr Ser Asn Thr Glu Ile Pro Gly His Ile Arg Lys Phe Phe Pro Ala  
 50 55 60 65  
 ttt cac gga act aag act att gag gcg tct gat gga tcg ggt cct caa 358  
 Phe His Gly Thr Lys Thr Ile Glu Ala Ser Asp Gly Ser Gly Pro Gln

	70	75	80	
cct cac ctg gtt ctg gag gat ctc gtc tcg ggt cgc acg aac cca tct				406
Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro Ser	85	90	95	
ctc atg gac atc aag act gga tcc aga aca tgg tat ccg gag gcc tct				454
Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala Ser	100	105	110	
gag gag tac atc caa aag tgc tta gag aaa gat cga aat agc aca agc				502
Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr Ser	115	120	125	
gtt tca ttg ggt ttt agg att tct ggg cta agg gta tat caa aat agc				550
Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn Ser	130	135	140	145
gaa gct gga ttt tgg caa cct gag aag aag gtt gtt tat agc ttt aat				598
Glu Ala Gly Phe Trp Gln Pro Glu Lys Lys Val Val Tyr Ser Phe Asn	150	155	160	
gcg gac ggt gtc agg tcg gct ctg agg aag ttt gtt tct tcc aac ttg				646
Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn Leu	165	170	175	
tct ctg ggt cca aat gtg gat ccg gat tgt ttg tat gca tca aaa gtt				694
Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys Val	180	185	190	
tac tgt cac cgg ggt gga att ttg gca caa ttg ctt cag ctg aag gaa				742
Tyr Cys His Arg Gly Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys Glu	195	200	205	
tggt ttt gag gtt cag acg aat tat cac ttc tat tct tgt tca ctc att				790
Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu Ile	210	215	220	225
atc tta tat gac agg gag tct gct ttg gac ggc tgt gca cac ccg aaa				838
Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro Lys	230	235	240	
gtt aaa ctg gtg gac ttt gca cat gtg atg gat ggc cac ggc gtg atc				886
Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val Ile	245	250	255	
gat cac aac ttc ttg ggt ggc ctc tgt tct gta atc aag ttt ata cgt				934
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Val Ile Lys Phe Ile Arg	260	265	270	
gac att gct gat gaa gat aac aag tgt gca aag tgc gaa gtc aat ctt				982
Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn Leu	275	280	285	
gga ttg aaa gaa aat ggc ttc tat aag agc agc acg gaa cca gag ctt				1030
Gly Leu Lys Glu Asn Gly Phe Tyr Lys Ser Ser Thr Glu Pro Glu Leu	290	295	300	305

gat cac gag gcc tgc tag tggaaactgg agaataactg cattcatgca  
 Asp His Glu Ala Cys \*  
 310

1078

ttcttcgatt cctgctctga caagtgggtc agaatgggta taataacagt ctattttagt 1138  
 caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1195

<210> 12  
 <211> 310  
 <212> PRT  
 <213> Eucalyptus grandis

<400> 12  
 Met Leu Lys Val Pro Asp His Gln Val Ala Gly His Arg Gly Asp Gly  
 1 5 10 15  
 Gly Lys Leu Gly Pro Leu Val Asp Asp Ser Gly Arg Phe Tyr Lys Pro  
 20 25 30  
 Leu Gln Ser Asp His Arg Gly Asp Thr Glu Val Ala Phe Tyr Glu Ser  
 35 40 45  
 Phe Tyr Ser Asn Thr Glu Ile Pro Gly His Ile Arg Lys Phe Phe Pro  
 50 55 60  
 Ala Phe His Gly Thr Lys Thr Ile Glu Ala Ser Asp Gly Ser Gly Pro  
 65 70 75 80  
 Gln Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro  
 85 90 95  
 Ser Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala  
 100 105 110  
 Ser Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr  
 115 120 125  
 Ser Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn  
 130 135 140  
 Ser Glu Ala Gly Phe Trp Gln Pro Glu Lys Lys Val Val Tyr Ser Phe  
 145 150 155 160  
 Asn Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn  
 165 170 175  
 Leu Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys  
 180 185 190  
 Val Tyr Cys His Arg Gly Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys  
 195 200 205  
 Glu Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu  
 210 215 220  
 Ile Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro  
 225 230 235 240  
 Lys Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val  
 245 250 255  
 Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Val Ile Lys Phe Ile  
 260 265 270  
 Arg Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn  
 275 280 285  
 Leu Gly Leu Lys Glu Asn Gly Phe Tyr Lys Ser Ser Thr Glu Pro Glu  
 290 295 300  
 Leu Asp His Glu Ala Cys  
 305 310

<210> 13  
 <211> 1020  
 <212> DNA

10042394.010902

<213> Parthenium argentatum

<220>

<221> CDS

<222> (21)...(908)

<400> 13

gcacgagaac ttcttcagac atg ctc aag gcc cca gat cat cag gtt gct gga	53
Met Leu Lys Ala Pro Asp His Gln Val Ala Gly	
1 5 10	
cat gaa gct ggg ctc ggg aag ctt ggc cca ctc att gat gat tca ggc	101
His Glu Ala Gly Leu Gly Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly	
15 20 25	
cgg ttt tac aaa cca ctg cag ggt gat aac cgt ggg tca gaa gaa gta	149
Arg Phe Tyr Lys Pro Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val	
30 35 40	
gcc ttt tat gaa tca ttt tct tct aac aat aat att cca gaa cac ata	197
Ala Phe Tyr Glu Ser Phe Ser Ser Asn Asn Asn Ile Pro Glu His Ile	
45 50 55	
cgc aaa ttc ttt cct ata tat tat ggc acc aaa atc atg aag gca tcc	245
Arg Lys Phe Phe Pro Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser	
60 65 70 75	
act ggc tct gac cat cct cac atg gtg ttg caa gat ctt aca tca gct	293
Thr Gly Ser Asp His Pro His Met Val Leu Gln Asp Leu Thr Ser Ala	
80 85 90	
cat gtc aac cca tct gta atg gac atc aaa atc ggg tcc aga aca tgg	341
His Val Asn Pro Ser Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp	
95 100 105	
gcg cca gaa gct tcc gag gcg tac att gca aaa tgc tta aaa aag gat	389
Ala Pro Glu Ala Ser Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp	
110 115 120	
agg gaa agc aca agt att cca ttg gga ttc agg atc tcc ggg ctg caa	437
Arg Glu Ser Thr Ser Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln	
125 130 135	
gtc tat atc gat gat ggg tca ggg ttt tat aag cct cat aga aat tac	485
Val Tyr Ile Asp Asp Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr	
140 145 150 155	
atg cgt aaa acc ggc cca gct gat gtt aga cta ctt ctt agg aaa ttt	533
Met Arg Lys Thr Gly Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe	
160 165 170	
gtt tct tct aac ccg tct gca gag atg gaa atg cgc aca ggc cta ggc	581
Val Ser Ser Asn Pro Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly	
175 180 185	
ccg gat tgt tct tta gca tct ttt gtt tat ggt ggg cct aat ggg ata	629
Pro Asp Cys Ser Leu Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile	
190 195 200	

10042894.010902

tta gct caa ctg atg gaa ttg aag aca tgg ttt gaa gat caa aca att 677  
 Leu Ala Gln Leu Met Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile  
 205 210 215  
 tac cac ttc tat gct tgt tct ttt ttg ttc atc ttt gaa aag agg ttg 725  
 Tyr His Phe Tyr Ala Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu  
 220 225 230 235  
 gtg tta aaa ggt gct cgg tca aac gca gaa gtc aaa ctt att gat ttt 773  
 Val Leu Lys Gly Ala Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe  
 240 245 250  
 gct cat gtt aca gat ggt aat ggt gtt att gat cac aat ttc ttg ggt 821  
 Ala His Val Thr Asp Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly  
 255 260 265  
 ggg ctc tgt tct ttg ata aag ttc att tct gac ata ctt tcg gag aca 869  
 Gly Leu Cys Ser Leu Ile Lys Phe Ile Ser Asp Ile Leu Ser Glu Thr  
 270 275 280  
 aaa gat tgt aat ggt aca aac ggt cag gtt gaa ctt tga aactctcttc 918  
 Lys Asp Cys Asn Gly Thr Asn Gly Gln Val Glu Leu \*  
 285 290 295  
 ttgtgtcttt tcttcaataa tttatcatga cagtgtttaa ttgtaaagat attcgcttac 978  
 cggaatatat ctgtgttatg agtgaaaaaa aaaaaaaaaa aa 1020  
 <210> 14  
 <211> 295  
 <212> PRT  
 <213> Parthenium argentatum  
 <400> 14  
 Met Leu Lys Ala Pro Asp His Gln Val Ala Gly His Glu Ala Gly Leu  
 1 5 10 15  
 Gly Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly Arg Phe Tyr Lys Pro  
 20 25 30  
 Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val Ala Phe Tyr Glu Ser  
 35 40 45  
 Phe Ser Ser Asn Asn Asn Ile Pro Glu His Ile Arg Lys Phe Phe Pro  
 50 55 60  
 Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser Thr Gly Ser Asp His  
 65 70 75 80  
 Pro His Met Val Leu Gln Asp Leu Thr Ser Ala His Val Asn Pro Ser  
 85 90 95  
 Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp Ala Pro Glu Ala Ser  
 100 105 110  
 Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp Arg Glu Ser Thr Ser  
 115 120 125  
 Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln Val Tyr Ile Asp Asp  
 130 135 140  
 Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr Met Arg Lys Thr Gly  
 145 150 155 160  
 Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe Val Ser Ser Asn Pro  
 165 170 175  
 Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly Pro Asp Cys Ser Leu  
 180 185 190



Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile Leu Ala Gln Leu Met  
 195 200 205  
 Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile Tyr His Phe Tyr Ala  
 210 215 220  
 Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu Val Leu Lys Gly Ala  
 225 230 235 240  
 Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe Ala His Val Thr Asp  
 245 250 255  
 Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu  
 260 265 270  
 Ile Lys Phe Ile Ser Asp Ile Leu Ser Glu Thr Lys Asp Cys Asn Gly  
 275 280 285  
 Thr Asn Gly Gln Val Glu Leu  
 290 295

<210> 15  
 <211> 899  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (89)...(424)

<400> 15  
 gccccaaaat ctcttttctcc gctgcgcgcg aaacccacgc ctccaccat cgccaccggt 60  
 caccctctgc tcccatagtc ccataacc atg ccc gac ctc cac ccg ccg gag 112  
 Met Pro Asp Leu His Pro Pro Glu  
 1 5

cac caa gtc gcc ggt cac cgc gcc tcc gcc agc aag ctg ggc cca ctc 160  
 His Gln Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu  
 10 15 20

atc gac ggc tct ggc ctc ttc tac aag ccg ctc cag gcc ggc gac cgt 208  
 Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg  
 25 30 35 40

ggg gag cac gag gtc gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc 256  
 Gly Glu His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala  
 45 50 55

gtc ccg gcc cgc atc cga gac acc ttc ttc ccc ccg ttc cac ggc acg 304  
 Val Pro Ala Arg Ile Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr  
 60 65 70

cga ctc ctc ccc acc gag gcg cag ccc ggg gag ccg cat ccg tac ctc 352  
 Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly Glu Pro His Pro Tyr Leu  
 75 80 85

gtc ctc gac gac ctc ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac 400  
 Val Leu Asp Asp Leu Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp  
 90 95 100

atc aag atc ggt gcc atc acg tga ccatgagcga tctgctcgga ttccacgtct 454  
 Ile Lys Ile Gly Ala Ile Thr \*  
 105 110

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ccggcgctccg agtcgtcggc cccgagggcg cgtgtgtggcg gacggagcgc cctgaggtga 514
aggctatgga cattgtcggc gtcgcgccgc tgctccggcg ctgcatgtca tccgcttgcc 574
ggcgagggga tggactcggc gctcgcggcg gcgtgtacg gaggaaaagg tggagtcttg 634
tcacagctgc gcgagctcaa ggcgtggttc gaggggcaga ctctgttcca ctctactcg 694
gcgtcgattc ttctgggcta tgatgtgtct gcagtcgag caggcggagg tgggggtggg 754
gtaacagtag agctgggtga ccttgcccat tgggcggagg gtgatggggt gattgaccac 814
aacttcctgg gcgggctctg ctatgtgatc aagtttgttt ctgacattgt tccagagact 874
ccttagacgc agcaaggcg aattc 899

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<210> 16
<211> 111
<212> PRT
<213> Zea mays

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<400> 16
Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
1 5 10 15
Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
20 25 30
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
35 40 45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
50 55 60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
65 70 75 80
Pro Gly Glu Pro His Pro Tyr Leu Val Leu Asp Asp Leu Leu Ala Gly
85 90 95
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr
100 105 110

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<210> 17
<211> 643
<212> DNA
<213> Zea mays

```

```

<220>
<221> misc_feature
<222> (1)...(643)
<223> n = A,T,C or G

```

```

<400> 17
ggcgcgtccct gntttttgta accaccocgc cccaaaaatct ctttctccgc tgcgtgcgaa 60
accacgcgct tccacatcgc ccaactcgta ccccttgctc ccatagtccc cataccatgc 120
cgcagctcca cccgcgggag caccgaagtc cgggtcaccg cgcctccgcc agcaagctgg 180
cccgctcat cgacggtctc ggctctttct acaagcgcgt ccaggcggcg gacggtgggg 240
agcacagagt cgcttctat gaggcgttct cgcgccacgc cgcgcgtccc gcccgcatcc 300
gagacacctt ctccccccgg ttccacggca cgcgactcct ccccaccgag gcgcagcccc 360
gggagcgcga tccgcacctc gtccctcgag acctcctcgc ggggttttag gcgcctcgcg 420
tcgcagacat ccaagatcgcc gccatcacgt ggccaccgag ttccgcggag cccatcatcg 480
ncaagtacct ngccaaaggac cgcgggacca cgagcgttct gtcgggattc cgcgtcttgc 540
gtccagatcg tccggcccgca ggggcggctg tggcggaacg agcgcgccgg ggggtgaangc 600
tatggacacc cgtcggngnc cggcgngtgc ttcggngnct acg 643

```

```

<210> 18
<211> 519
<212> DNA

```

<213> Zea mays

<220>

<221> misc\_feature

<222> (1) ... (519)

<223> n = A,T,C or G

<400> 18

ggtaacggang	aaaangtgga	gtcttgctac	agctgcgcga	gtccaangcg	tggttcgagg	60
ggcagactct	gttccacttc	tactcggcgt	cgattcttct	gggctatgat	gctgctgcag	120
tcgcagcagg	cggaangtggg	gggtggggtaa	cagtgaaagct	gggtgaacttt	gcccatgtgg	180
ccgagggtga	tggggtgatt	gaccacaact	tcctggggcgg	gctcgtctan	ctgatcaagt	240
ttgtttctga	cattgttcca	gagactcctc	agacgcagcc	tttgggtctc	tcttaagaaa	300
agatcctggc	attttcgatt	tgataacaaa	ggaanacact	tcagctgccca	aaaaaaaanc	360
accagtgaag	atgaaaaata	cattattgag	gaaagtccg	atnataaccc	accanattna	420
aaaaaaaaag	gtcccaaat	tcgaaaatn	tggaatctaa	gaataatctc	ctgaaaacan	480
aattataaaa	cgtgaaaacc	ccggctnctn	catttacnc			519

<210> 19

<211> 353

<212> DNA

<213> Zea mays

<220>

<221> misc\_feature

<222> (1) ... (353)

<223> n = A,T,C or G

<400> 19

ctcaaggcat	gggtggagga	gcagaactctg	ttccaacttct	actcggcgctc	gattcttctg	60
ggctatgatg	ctgctgcagt	cgcancaggc	ggaggtgggg	gtggggtaac	agtgaagctg	120
gtggactttg	cccattgtggc	cgagggtgat	gggggttgatt	tgaccacaac	ttcctggggc	180
agctctgcta	gtgatacaag	ttccgtttct	tgacattgtt	ccaganaactc	cttagacgcc	240
agcctttggg	tccttcctta	aaaaaagatc	cctgaenctt	ttgatttgat	tacnaaggaa	300
acactttcca	cttgccnaaa	aaaaaagccc	ntgaggatta	aaaaattaac	ntt	353

<210> 20

<211> 3416

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (72) ... (407)

<400> 20

ccacgcgtcc	ggcaaaccca	ccgcttccac	catcgccacc	cgtcacccct	tgctcccata	60
gtccccatac	c atg ccc gac ctc cac	ccg ccg gag cac caa gtc gcc ggt				110
	Met Pro Asp Leu His	Pro Pro Glu His	Gln Val Ala Gly			
	1	5	10			
cac cgc gcc tcc gcc	agc aag ctg ggc cca ctc	atc gac gac tct ggc				158
His Arg Ala Ser Ala	Ser Lys Leu Gly	Pro Leu Ile Asp Asp Ser Gly				
	15	20	25			
ctc ttc tac aag ccg ctc	cag gcc ggc gac cgt	ggg gag cac gag gtc				206
Leu Phe Tyr Lys Pro	Leu Gln Ala Gly Asp Arg	Gly Glu His Glu Val				
	30	35	40			45

gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc gtc cgg gcc cgc atc 254  
Ala Phe Tyr Glu Ala Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile  
50 55 60

cga gac acc ttc ttc ccc cgg ttc cac gcc acg cga ctc ctc ccc acc 302  
Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr  
65 70 75

gag gcg cag ccc ggg gag cgg cat cgg cac ctc gtc ctc gac gac ctc 350  
Glu Ala Gln Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu  
80 85 90

ctc cgg ggg ttt gag gcg ccc tgc gtc gca gac atc aag atc ggt gcc 398  
Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala  
95 100 105

atc acg tga ccaacgagcgt tctgctcgga ttccgcgtct ccggcgctccg 447  
Ile Thr \*  
110

agtcgtcgcc ccgagggcg ccgtgtggcg gacggagcgc ccggagggtga aggcctatgga 507  
cattgtcgcc gtcgcgcggc gtctccggcg ctacgtgtca tccgcgttgc gacgagggga 567  
tggactgcgc gctcgcggcg cgggtgtacg gaggaaaagg tggagctctg tcacagctgc 627  
gcgagctcaa ggcgtgggttc gaggggcaga ctctgttcca ctctactcgc gcgtcgatc 687  
ttctgggcta tgatgctgct gcagtcgcag caggcggagg tgggggtggg gtaacagta 747  
agctgggtga ctttggccat gtggcggagg gtgatgggt gattgaccac aacttccctgg 807  
gcgggctctg ctactgtatc aagttgttt ctgacattgt tccagagact cctcagacgc 867  
agcctttggg tcctctctaa gagaggatcc tggcattttc gatttgatac caaagggaagc 927  
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<212> PRT
<213> Zea mays

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Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
35 40 45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
50 55 60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
65 70 75 80
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<222> (52)...(1020)

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Pro Ala Pro Ala Val Pro Asn Gly Thr Gly Ala Pro Leu Lys Asp Glu
5 10 15
cct tcc aac ccc gat cag gcg cag cac cag cct gac gag cgc gtt caa 153
Pro Ser Asn Pro Asp Gln Ala Gln His Gln Pro Asp Glu Arg Val Gln
20 25 30

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cac ttc atc ctt ctt gaa gac ctt act gct ggc atg aca agg cct tgt 201  
 His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg Pro Cys  
 35 40 45 50  
 gtc tta gac ttg aag atg ggt acg cgc cag tat ggt gtg gaa gcc gat 249  
 Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu Ala Asp  
 55 60 65  
 gag aag aaa cag cgg tct caa cgg cgc aag tgt cag atg acc acc agt 297  
 Glu Lys Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr Thr Ser  
 70 75 80  
 gct caa ctc ggc gtg cga gtc tgc ggt atg caa att tgg aac gcc aag 345  
 Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn Ala Lys  
 85 90 95  
 acc cag agc tac atc ttc gag gac aag tac ttc ggt cga gat ctg aaa 393  
 Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp Leu Lys  
 100 105 110  
 gca gga aaa gaa ttt cag gac gcg ctt aag cgc ttt ttt tgg gat ggg 441  
 Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp Asp Gly  
 115 120 125 130  
 acg agc tac aaa gca gca aac aga cac ata ccc gtc ata ttg gag aag 489  
 Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu Glu Lys  
 135 140 145  
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 Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr Arg Phe  
 150 155 160  
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 Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly Glu Ser  
 165 170 175  
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 180 185 190  
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 Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser Pro Gly  
 195 200 205 210  
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 Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu Ile Lys  
 215 220 225  
 ctg aaa att gtc gac ttt gcc aac tgc gtg act gca gaa gac cct cta 777  
 Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp Pro Leu  
 230 235 240  
 cca gac gac tta cct tgt cca cct gaa aat ccc gac ggc atc gat aga 825  
 Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile Asp Arg  
 245 250 255  
 ggg tac ctc cgt ggc ctc cga tca cta cgc ctc tac ttc caa cgc att 873  
 Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln Arg Ile  
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atg gcg cga aat cat cac cat ggc cct ggt tta ggt gag gtt ggt gcg			969
Met Ala Arg Asn His His Gly Pro Gly Leu Gly Glu Val Gly Ala			
295 300 305			
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Gly Trp Met Asp Asp Ala Gly Gly Glu Asp Thr Gly Tyr Ala Ser Phe			
310 315 320			
taa agaagaggag gaacagcaaa gctgcccacg ctgcacagaa gtcggacagt			1070
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35 40 45			
Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu			
50 55 60			
Ala Asp Glu Lys Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr			
65 70 75 80			
Thr Ser Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn			
85 90 95			
Ala Lys Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp			
100 105 110			
Leu Lys Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp			
115 120 125			
Asp Gly Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu			
130 135 140			
Glu Lys Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr			
145 150 155 160			
Arg Phe Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly			
165 170 175			
Glu Ser Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser			
180 185 190			
Asn Pro Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser			
195 200 205			

Pro Gly Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu  
 210 215 220  
 Ile Lys Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp  
 225 230 235 240  
 Pro Leu Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile  
 245 250 255  
 Asp Arg Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln  
 260 265 270  
 Arg Ile Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly  
 275 280 285  
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 Gly Ala Gly Trp Met Asp Asp Ala Gly Gly Glu Asp Thr Gly Tyr Ala  
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 Ser Phe

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 Phe Gln Thr Tyr Lys Lys Gln Arg Tyr Pro Trp Val Gln Leu Ala Gly  
 20 25 30  
 cac caa ggc aat ttc aaa gcc ggt ccg gaa cct ggt acg atc ctc aag 143  
 His Gln Gly Asn Phe Lys Ala Gly Pro Glu Pro Gly Thr Ile Leu Lys  
 35 40 45  
 aaa ctt tgt ccc aaa gaa cag ttg tgc ttc caa gtg ctg atg aag gac 191  
 Lys Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp  
 50 55 60  
 gtt ctg aga ccg tac gtg ccc gaa tac aag ggc cac ttg act acc gac 239  
 Val Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp  
 65 70 75  
 gac gga gac cta tat ctt cag cta gaa gac ttg ttg ggt gac ttc act 287  
 Asp Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr  
 80 85 90 95  
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 Ser Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu  
 100 105 110  
 gag gaa ctg gcg aaa gcc aaa gag aaa ccc aag ttg aga aaa gac atg 383  
 Glu Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met



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gag tgg gtg gtg ggc aac cac gag gac ggt tac ctg atc ggt atc aac Glu Trp Val Val Gly Asn His Glu Asp Gly Tyr Leu Ile Gly Ile Asn 275 280 285			863
aac ctg ctg gac ata ttc acc gat atg aac gcc gcc acc gcg ttt ccc Asn Leu Leu Asp Ile Phe Thr Asp Met Asn Ala Ala Thr Ala Phe Pro 290 295 300			911
gtc acg ctc atc gaa gtc acg gcc ccg tcc gaa gtc acc tga Val Thr Leu Ile Glu Val Thr Ala Pro Ser Glu Val Thr * 305 310 315			953
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 <213> Zea mays

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 Gln Gly Asn Phe Lys Ala Gly Pro Glu Pro Gly Thr Ile Leu Lys Lys  
 35 40 45  
 Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp Val  
 50 55 60  
 Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp Asp  
 65 70 75 80  
 Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr Ser  
 85 90 95  
 Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu Glu  
 100 105 110  
 Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met Tyr  
 115 120 125  
 Glu Lys Met Ile Gln Ile Asp Pro Asn Ala Pro Ser Glu Glu Glu His  
 130 135 140  
 Arg Leu Lys Gly Val Thr Lys Pro Arg Tyr Met Val Trp Arg Glu Thr  
 145 150 155 160  
 Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys Lys  
 165 170 175  
 Ser Asp Gly Lys Ser Ser Lys Asp Phe Lys Thr Thr Lys Asn Arg Asp  
 180 185 190  
 Gln Val Ile Glu Ala Phe Arg Asp Phe Val Ala Gly Phe Pro His Val  
 195 200 205  
 Ile Pro Lys Tyr Ile Asn Arg Leu Arg Ala Ile Arg Asp Ile Leu Val  
 210 215 220  
 Asn Ser Lys Phe Phe Thr Thr His Glu Val Ile Gly Ser Ser Leu Leu  
 225 230 235 240  
 Phe Val His Asp Ser Lys Asn Ala Asn Ile Trp Leu Ile Asp Phe Ala  
 245 250 255  
 Lys Thr Leu Ile Leu Pro Pro Asp Ile Arg Ile Asn His Thr Ser Glu  
 260 265 270  
 Trp Val Val Gly Asn His Glu Asp Gly Tyr Leu Ile Gly Ile Asn Asn  
 275 280 285  
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290 295 300  
Thr Leu Ile Glu Val Thr Ala Pro Ser Glu Val Thr  
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<210> 26  
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<212> PRT  
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Leu Lys Xaa Pro Glu His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly  
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<210> 31  
<211> 33  
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<220>  
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Gln

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20 25 30  
Gln

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 20 25 30  
 Gln

<210> 34  
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<221> VARIANT  
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 20 25 30  
 Ile Xaa Lys Cys Leu Xaa Lys Asp Arg  
 35 40

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<400> 35

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Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Ser Val Met Asp  
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 35 40

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 Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Cys Val Met Asp  
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 Val Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr  
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 Ile Xaa Lys Cys Leu Xaa Lys Asp Arg  
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<220>  
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<221> VARIANT  
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 Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Cys Val Met Asp  
 1 5 10 15  
 Ile Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr  
 20 25 30  
 Ile Xaa Lys Cys Leu Xaa Lys Asp Arg  
 35 40